```
                .         .         .         .         .         .
  1 CCCACGCGTCCGGCCCGCCGGCTCCGGAGCGGCTCTGCCTTCCCGAGCGCGGGACGCGGC  60

                .         .         .         .         .         .
 61 GCCCTGGGGGAGGAGGGCGAAGCGACGCGGCGATGGCTCCGCGGGCACTCCCGGGGTCCG 120
  1                                 M  A  P  R  A  L  P  G  S  A  10

                .         .         .         .         .         .
121 CCGTCCTAGCCGCTGCTGTCTTCGTGGGAGGCGCCGTGAGTTCGCCGCTGGTGGCTCCGG 180
 11   V  L  A  A  A  V  F  V  G  G  A  V  S  S  P  L  V  A  P  D  30

                .         .         .         .         .         .
181 ACAATGGGAGCAGCCGCACATTGCACTCCAGAACAGAGACGACCCCGTCGCCCAGCAACG 240
 31   N  G  S  S  R  T  L  H  S  R  T  E  T  T  P  S  P  S  N  D  50

                .         .         .         .         .         .
241 ATACTGGGAATGGACACCCAGAATATATTGCATACGCGCTTGTCCCTGTGTTCTTTATCA 300
 51   T  G  N  G  H  P  E  Y  I  A  Y  A  L  V  P  V  F  F  I  M  70

                .         .         .         .         .         .
301 TGGGTCTCTTTGGCGTCCTCATTTGCCACCTGCTTAAGAAGAAAGGCTATCGTTGTACAA 360
 71   G  L  F  G  V  L  I  C  H  L  L  K  K  K  G  Y  R  C  T  T  90

                .         .         .         .         .         .
361 CAGAAGCAGAGCAAGATATCGAAGAGGAAAAGGTTGAAAAGATAGAATTGAATGACAGTG 420
 91   E  A  E  Q  D  I  E  E  E  K  V  E  K  I  E  L  N  D  S  V 110

                .         .         .         .         .         .
421 TGAATGAAAACAGTGACACTGTTGGGCAAATCGTCCACTACATCATGAAAAATGAAGCGA 480
111   N  E  N  S  D  T  V  G  Q  I  V  H  Y  I  M  K  N  E  A  N 130

                .         .         .         .         .         .
481 ATGCTGATGTCTTAAAGGCGATGGTAGCAGATAACAGCCTGTATGATCCTGAAAGCCCCG 540
131   A  D  V  L  K  A  M  V  A  D  N  S  L  Y  D  P  E  S  P  V 150

                .         .         .         .         .         .
541 TGACCCCCAGCACACCAGGGAGCCCGCCAGTGAGTCCTGGGCCTTTGTCACCAGGGGGGA 600
151   T  P  S  T  P  G  S  P  P  V  S  P  G  P  L  S  P  G  G  T 170

                .         .         .         .         .         .
601 CGCCAGGGAAGCACGTCTGTGGCCATCATCTGCATACGGTGGGCGGTGTTGTCGAGAGGG 660
171   P  G  K  H  V  C  G  H  H  L  H  T  V  G  G  V  V  E  R  D 190
```

FIG. 1A

```
661 ATGTGTGTCATCGGTGTAGGCACAAGCGGTGGCACTTTATAAAGCCCACTAACAAGTCCA 720
191   V  C  H  R  C  R  H  K  R  W  H  F  I  K  P  T  N  K  S  R 210

721 GAGAGAGCAGACCACGGCGCCAAGGCGAGGTCACGGTCCTTTCTGTTGGCAGATTTAGAG 780
211   E  S  R  P  R  R  Q  G  E  V  T  V  L  S  V  G  R  F  R  V 230

781 TTACAAAAGTGGAGCACAAGTCAAACCAGAAGGAACGGAGAAGCCTGATGTCTGTTAGTG 840
231   T  K  V  E  H  K  S  N  Q  K  E  R  R  S  L  M  S  V  S  G 250

841 GGGCTGAAACCGTCAATGGGGAGGTGCCGGCAACACCTGTGAAGAGAGAACGCAGTGGCA 900
251   A  E  T  V  N  G  E  V  P  A  T  P  V  K  R  E  R  S  G  T 270

901 CAGAGTAGCAGGTGAGCCGTGGTTTTGGTGACATTGGGGGCAGAGTGGTGCAGGGTGAGG 960
271   E  *                                                       272

961 AGAAGGTACTTGGAGCCTCCCAGGTGCTGTGGCAGCATAGGAATGGTATTTGACAGGGAA 1020

1021 GTGGGAGAGCTTTCCTTGACCCAGGAAGACTGAGGGGGACTGAACATGATTACTTGTCTG 1080

1081 CCTAGAGCTTCTTGTAAAGAAGTCACAAACTTAGTGCCTCCAGGGGCTTGGCCTGTGTGA 1140

1141 TAATGAGGATAGAGGATTACTTGTGAGGCAATGTGGCATGGTGGGGATTGTGGCAAACTA 1200

1201 GAATTCACATCACCCACCATATAGGGCTTGCATTACCACGAGGCAGAAAGCACCTAGTGT 1260

1261  TGCTGCATCTTCTTACGCAAAAAAAAAAAA                              1291
```

FIG. 1B

```
                .         .         .         .         .         .
  1 CGGACGCGTGGGGGGCTATATATGCTCTTCCTGCTTGTGCTGGTCTTCTTCCTCATGGGC  60
  1  R  T  R  G  G  L  Y  M  L  F  L  L  V  L  V  F  F  L  M  G   20

                .         .         .         .         .         .
 61 CTGGTAGGCTTCATGATCTGCCACGTGCTCAAGAAGAAGGGCTACCGCTGCCGCACGTCG 120
 21  L  V  G  F  M  I  C  H  V  L  K  K  K  G  Y  R  C  R  T  S   40

                .         .         .         .         .         .
121 AGGGGCTCTGAGCCTGACGATGCCCAGCTTCAGCCCCCTGAGGACGATGACATGAATGAG 180
 41  R  G  S  E  P  D  D  A  Q  L  Q  P  P  E  D  D  D  M  N  E   60

                .         .         .         .         .         .
181 GACACAGTAGAGAGGATTGTTCGCTGCATCATCCAGAATGAAGCCAATGCTGAGGCCTTG 240
 61  D  T  V  E  R  I  V  R  C  I  I  Q  N  E  A  N  A  E  A  L   80

                .         .         .         .         .         .
241 AAGGAGATGCTGGGGGACAGTGAAGGAGAAGGGACAGTGCAGCTGTCCAGTGTGGATGCC 300
 81  K  E  M  L  G  D  S  E  G  E  G  T  V  Q  L  S  S  V  D  A  100

                .         .         .         .         .         .
301 ACCTCCAGCCTGCAGGACGGAGCCCCCTCCCATCATCACACAGTGCACCTGGGCTCTGCA 360
101  T  S  S  L  Q  D  G  A  P  S  H  H  H  T  V  H  L  G  S  A  120

                .         .         .         .         .         .
361 GCCCCTTGCCTCCATTGCAGCCGCAGCAAGAGGCCTCCACTTGTCCGTCAGGGACGCTCC 420
121  A  P  C  L  H  C  S  R  S  K  R  P  P  L  V  R  Q  G  R  S  140

                .         .         .         .         .         .
421 AAGGAAGGAAAAAGCCGCCCCCGGACAGGGGAGACCACTGTGTTCTCTGTGGGCAGGTTC 480
141  K  E  G  K  S  R  P  R  T  G  E  T  T  V  F  S  V  G  R  F  160

                .         .         .         .         .         .
481 CGGGTGACACACATTGAGAAGCGCTATGGACTGCACGAACACCGTGATGGCTCCCCCACA 540
161  R  V  T  H  I  E  K  R  Y  G  L  H  E  H  R  D  G  S  P  T  180

                .         .         .         .
541 GACAGGAGCTGGGGCTCTGGTGGGGGACAGGACCCAGGGGTG                   582
181  D  R  S  W  G  S  G  G  G  Q  D  P  G  V                   194
```

FIG. 2

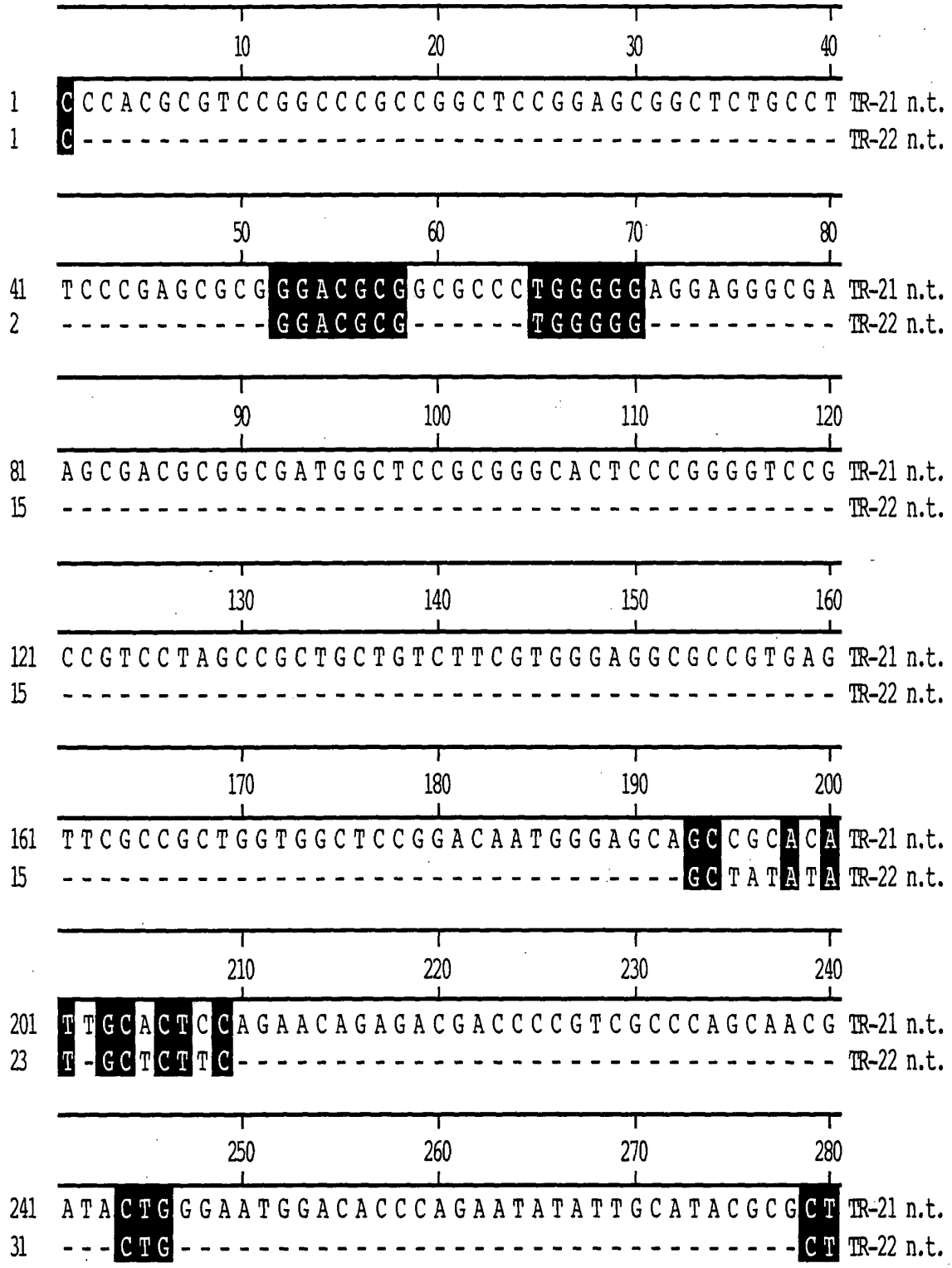

10 20 30 40
1 CCCACGCGTCCGGCCCGCCGGCTCCGGAGCGGCTCTGCCT TR-21 n.t.
1 C---------- TR-22 n.t.
50 60 70 80
41 TCCCGAGCGCGGGACGCGGCGCCCTGGGGGAGGAGGGCGA TR-21 n.t.
2 ----------GGACGCG-------TGGGGG---------- TR-22 n.t.
90 100 110 120
81 AGCGACGCGGCGATGGCTCCGCGGGCACTCCCGGGGTCCG TR-21 n.t.
15 ---------- TR-22 n.t.
130 140 150 160
121 CCGTCCTAGCCGCTGCTGTCTTCGTGGGAGGCGCCGTGAG TR-21 n.t.
15 ---------- TR-22 n.t.
170 180 190 200
161 TTCGCCGCTGGTGGCTCCGGACAATGGGAGCAGCCGCACA TR-21 n.t.
15 ----------GCTATATA TR-22 n.t.
210 220 230 240
201 TTGCACTCCAGAACAGAGACGACCCCGTCGCCCAGCAACG TR-21 n.t.
23 T-GCTCTTC---------- TR-22 n.t.
250 260 270 280
241 ATACTGGGAATGGACACCCAGAATATATTGCATACGCGCT TR-21 n.t.
31 ---CTG----------CT TR-22 n.t.

FIG. 3A

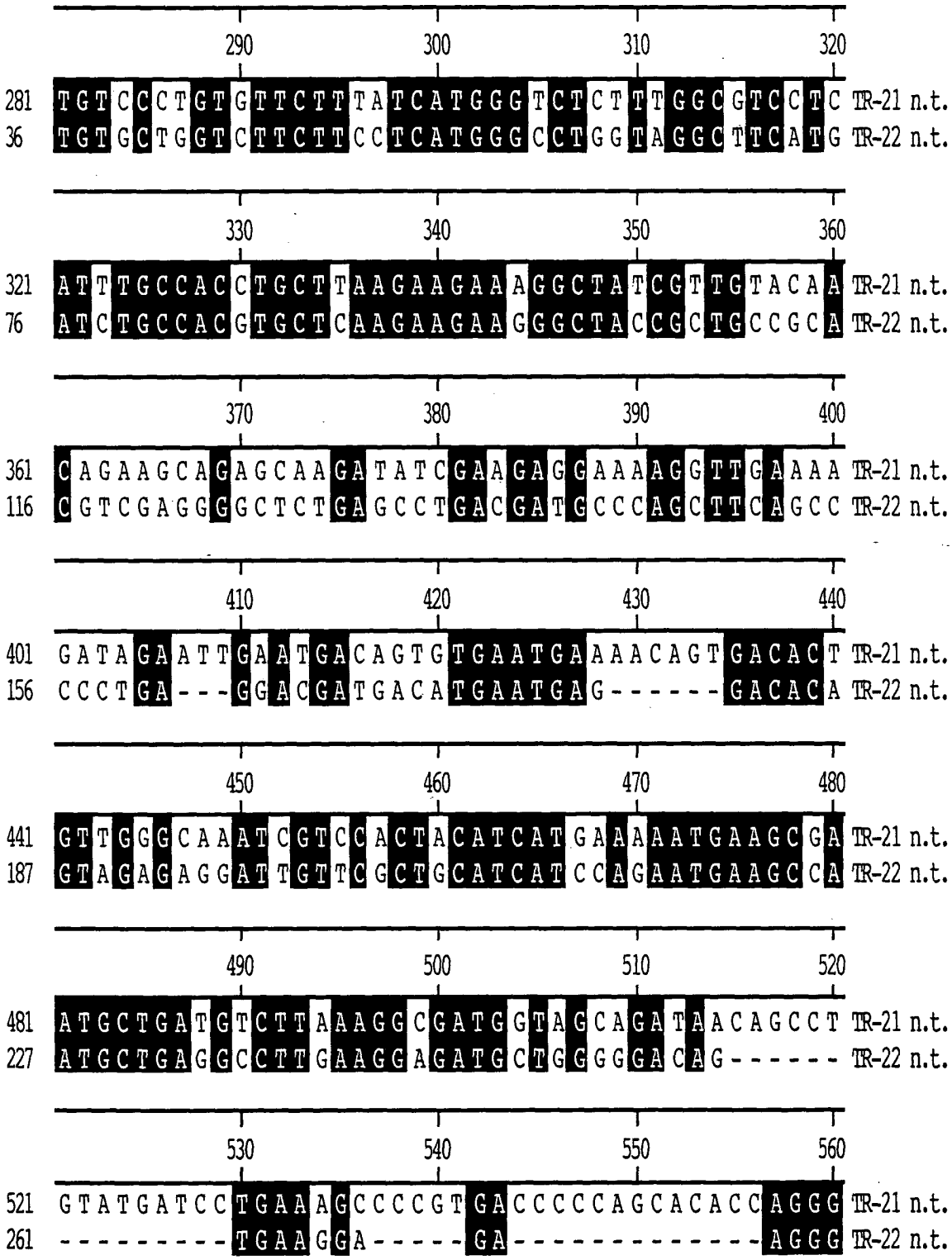

290 300 310 320
281 TGTCCCTGTGTTCTTTATCATGGGTCTCTTTGGCGTCCTC TR-21 n.t.
36 TGTGCTGGTCTTCTTCCTCATGGGCCTGGTAGGCTTCATG TR-22 n.t.
330 340 350 360
321 ATTTGCCACCTGCTTAAGAAGAAAGGCTATCGTTGTACAA TR-21 n.t.
76 ATCTGCCACGTGCTCAAGAAGAAGGGCTACCGCTGCCGCA TR-22 n.t.
370 380 390 400
361 CAGAAGCAGAGCAAGATATCGAAGAGGAAAAGGTTGAAAA TR-21 n.t.
116 CGTCGAGGGCTCTGAGCCTGACGATGCCCAGCTTCAGCC TR-22 n.t.
410 420 430 440
401 GATAGAATTGAATGACAGTGTGAATGAAAACAGTGACACT TR-21 n.t.
156 CCCTGA---GGACGATGACATGAATGAG------GACACA TR-22 n.t.
450 460 470 480
441 GTTGGGCAAATCGTCCACTACATCATGAAAAATGAAGCGA TR-21 n.t.
187 GTAGAGAGGATTGTTCGCTGCATCATCCAGAATGAAGCCA TR-22 n.t.
490 500 510 520
481 ATGCTGATGTCTTAAAGGCGATGGTAGCAGATAACAGCCT TR-21 n.t.
227 ATGCTGAGGCCTTGAAGGAGATGCTGGGGGACAG------ TR-22 n.t.
530 540 550 560
521 GTATGATCCTGAAAGCCCCGTGACCCCCAGCACACCAGGG TR-21 n.t.
261 ---------TGAAGGA-----GA----------AGGG TR-22 n.t.

FIG. 3B

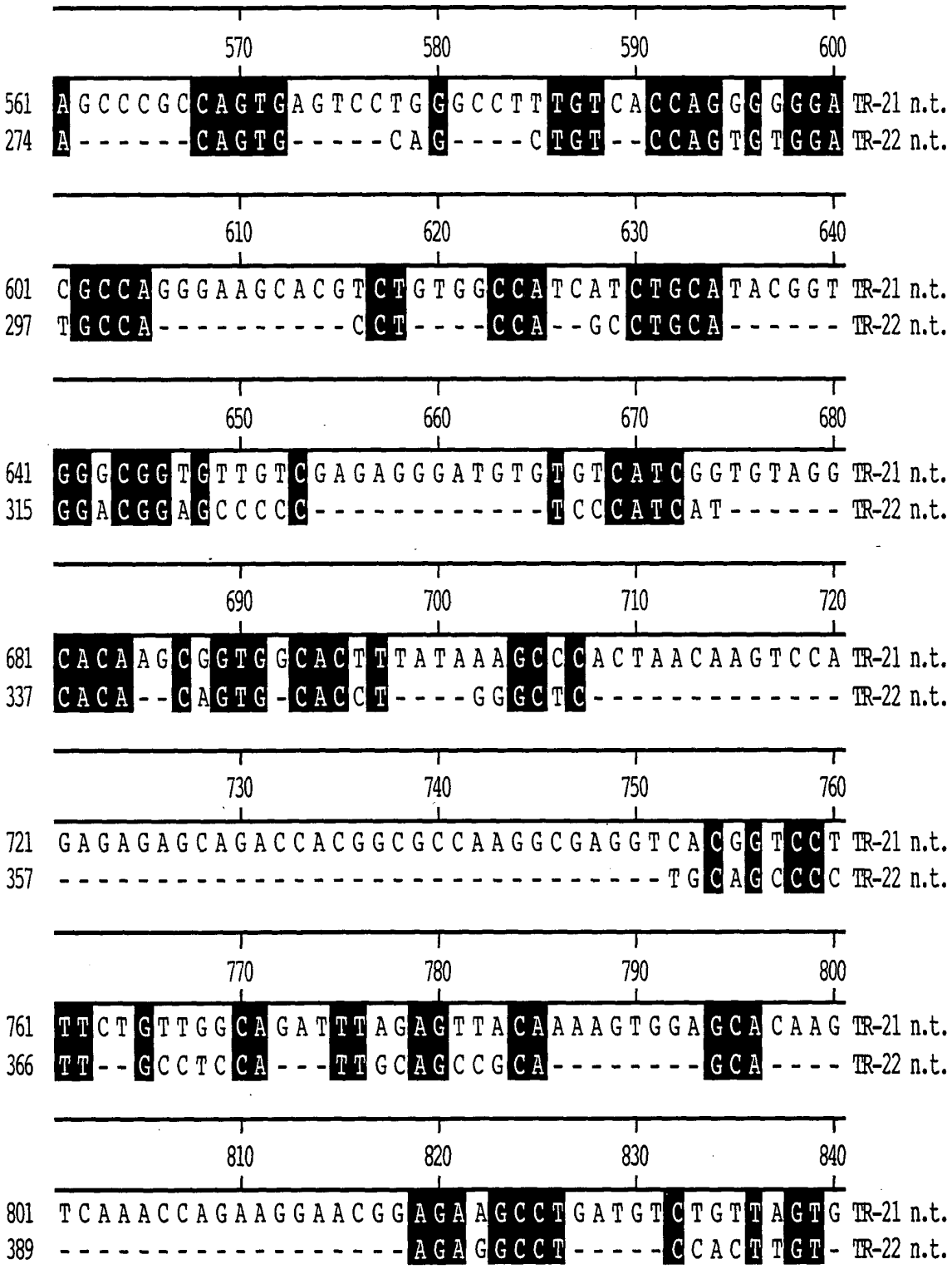

570 580 590 600
561 AGCCCGCCAGTGAGTCCTGGGCCTTTGTCACCAGGGGGGA TR-21 n.t.
274 A------CAGTG-----CAG----CTGT--CCAGTGTGGA TR-22 n.t.
610 620 630 640
601 CGCCAGGGAAGCACGTCTGTGGCCATCATCTGCATACGGT TR-21 n.t.
297 TGCCA----------CCT----CCA--GCCTGCA------ TR-22 n.t.
650 660 670 680
641 GGGCGGTGTTGTCGAGAGGGATGTGTGTCATCGGTGTAGG TR-21 n.t.
315 GGACGGAGCCCCC----------TCCCATCAT------ TR-22 n.t.
690 700 710 720
681 CACAAGCGGTGGCACTTTATAAAGCCCACTAACAAGTCCA TR-21 n.t.
337 CACA--CAGTG-CACCT----GGGCTC---------- TR-22 n.t.
730 740 750 760
721 GAGAGAGCAGACCACGGCGCCAAGGCGAGGTCACGGTCCT TR-21 n.t.
357 ----------TGCAGCCCC TR-22 n.t.
770 780 790 800
761 TTCTGTTGGCAGATTTAGAGTTACAAAAGTGGAGCACAAG TR-21 n.t.
366 TT--GCCTCCA---TTGCAGCCGCA--------GCA---- TR-22 n.t.
810 820 830 840
801 TCAAACCAGAAGGAACGGAGAAGCCTGATGTCTGTTAGTG TR-21 n.t.
389 ----------AGAGGCCT-----CCACTTGT- TR-22 n.t.

FIG. 3C

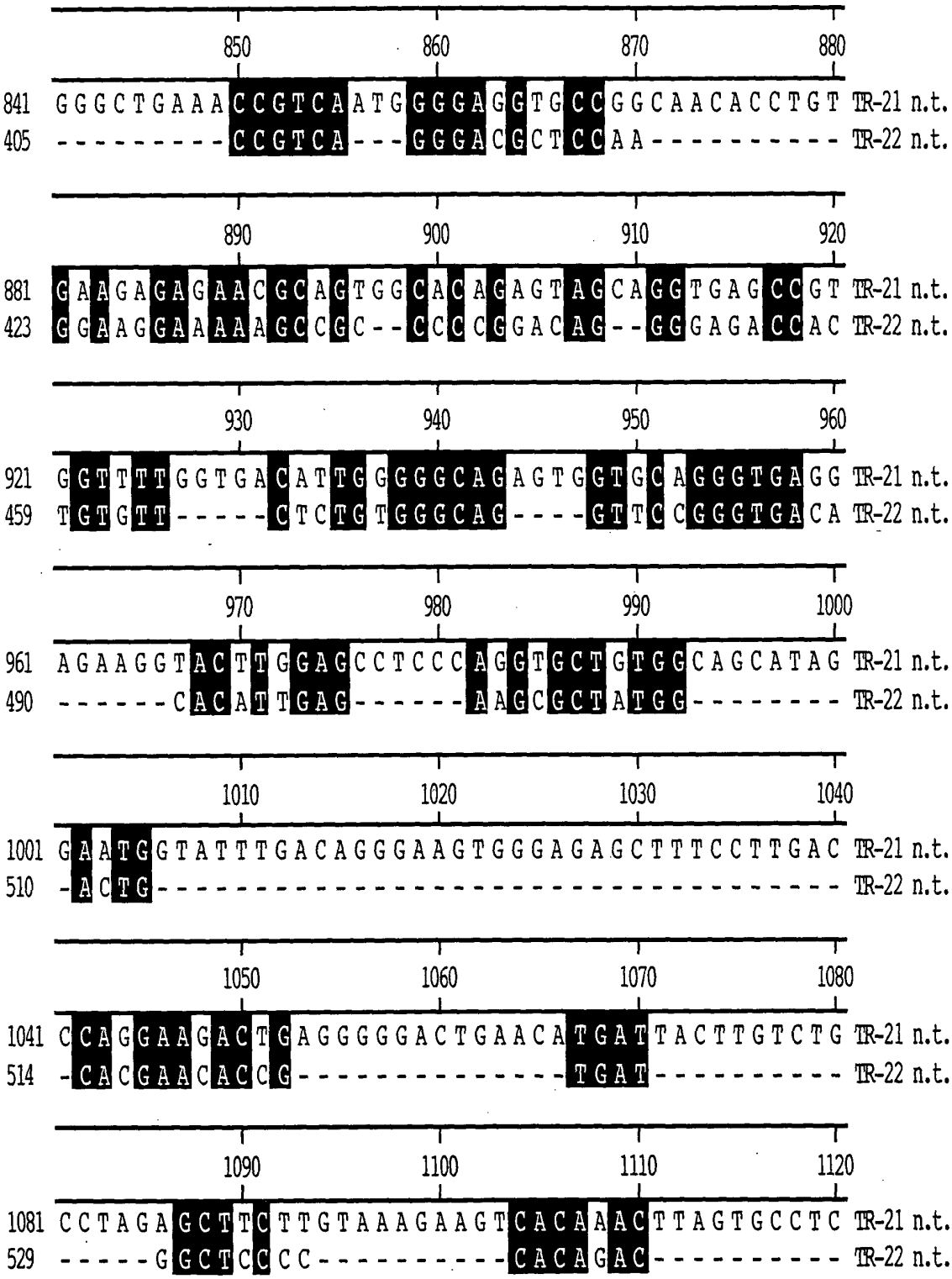
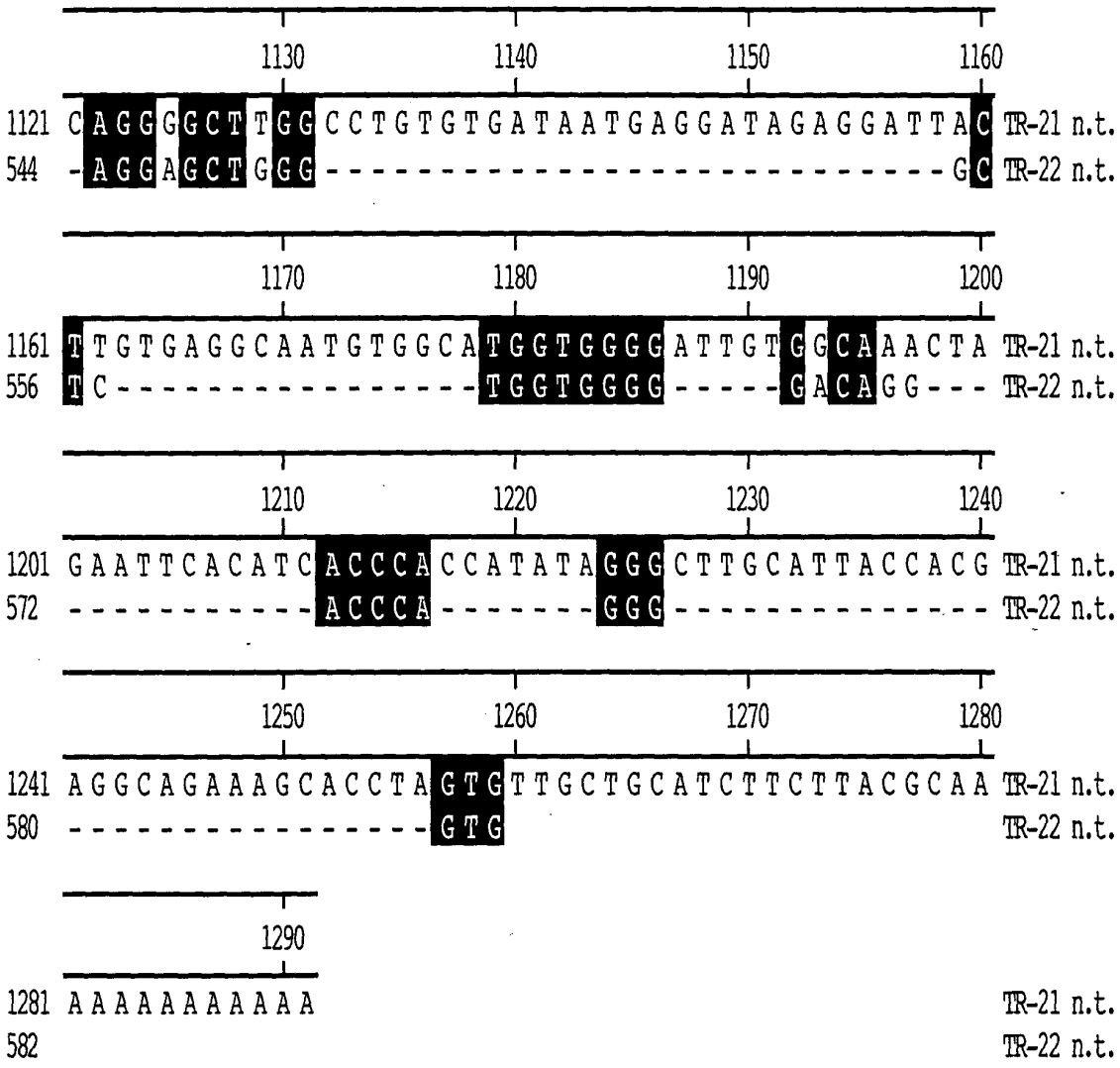
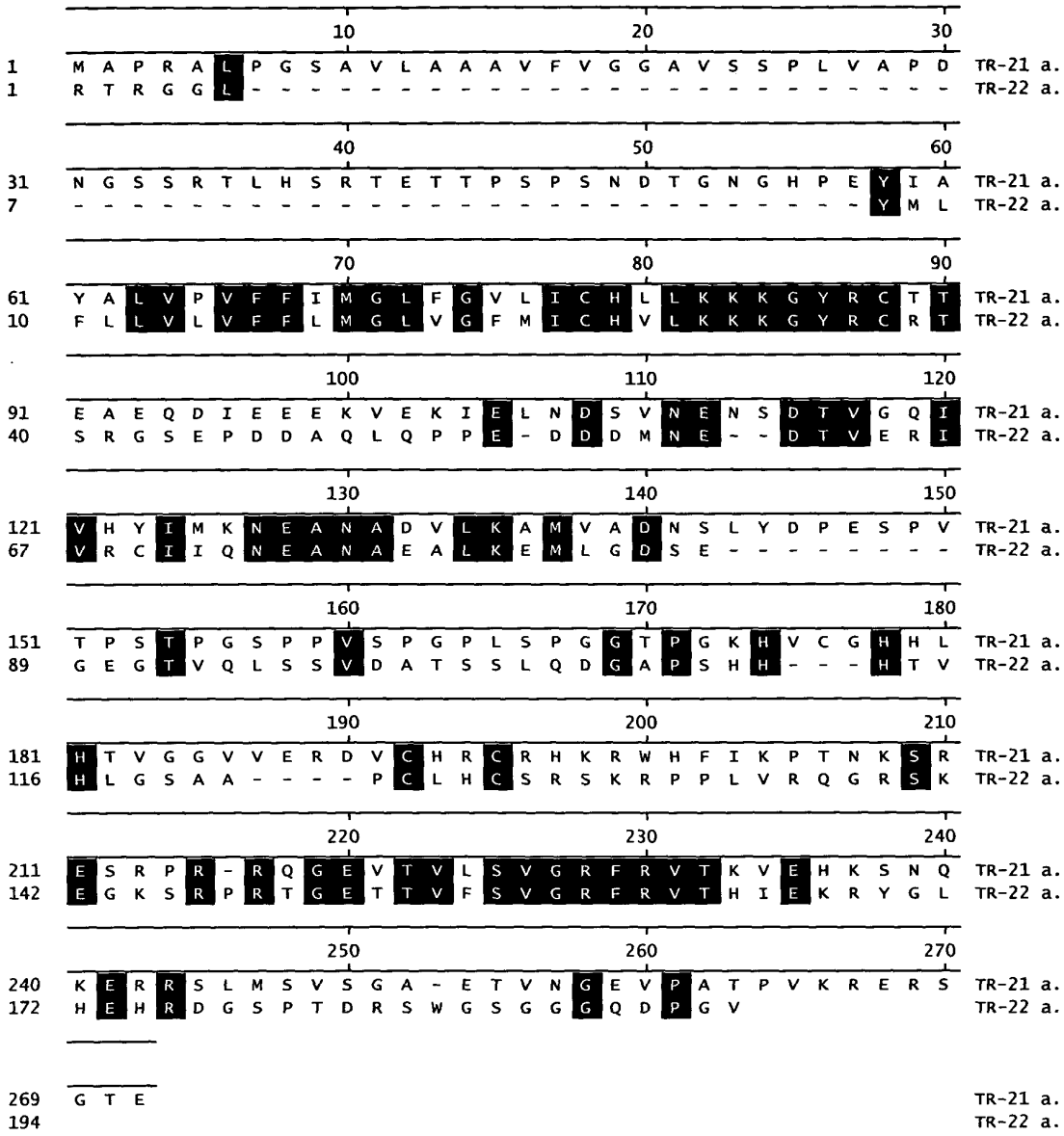

850 860 870 880
841 GGGCTGAAACCGTCAATGGGGAGGTGCCGGCAACACCTGT TR-21 n.t.
405 ----------CCGTCA---GGGACGCTCCAA---------- TR-22 n.t.
890 900 910 920
881 GAAGAGAGAACGCAGTGGCACAGAGTAGCAGGTGAGCCGT TR-21 n.t.
423 GGAAGGAAAAAGCCGC--CCCCGGACAG--GGGAGACCAC TR-22 n.t.
930 940 950 960
921 GGTTTTGGTGACATTGGGGGCAGAGTGGTGCAGGGTGAGG TR-21 n.t.
459 TGTGTT-----CTCTGTGGGCAG----GTTCCGGGTGACA TR-22 n.t.
970 980 990 1000
961 AGAAGGTACTTGGAGCCTCCCAGGTGCTGTGGCAGCATAG TR-21 n.t.
490 ------CACATTGAG------AAGCGCTATGG-------- TR-22 n.t.
1010 1020 1030 1040
1001 GAATGGTATTTGACAGGGAAGTGGGAGAGCTTTCCTTGAC TR-21 n.t.
510 -ACTG---------- TR-22 n.t.
1050 1060 1070 1080
1041 CCAGGAAGACTGAGGGGGACTGAACATGATTACTTGTCTG TR-21 n.t.
514 -CACGAACACCG----------TGAT---------- TR-22 n.t.
1090 1100 1110 1120
1081 CCTAGAGCTTCTTGTAAAGAAGTCACAAACTTAGTGCCTC TR-21 n.t.
529 -----GGCTCCCC----------CACAGAC---------- TR-22 n.t.

FIG. 3D



Decoration 'Decoration #1': Shade (with solid black) residues that match the consensus named 'Consensus #1' exactly.

FIG. 3E



Decoration 'Decoration #1': Shade (with solid black) residues that match the consensus named 'Consensus #1' exactly.♪

FIG. 4

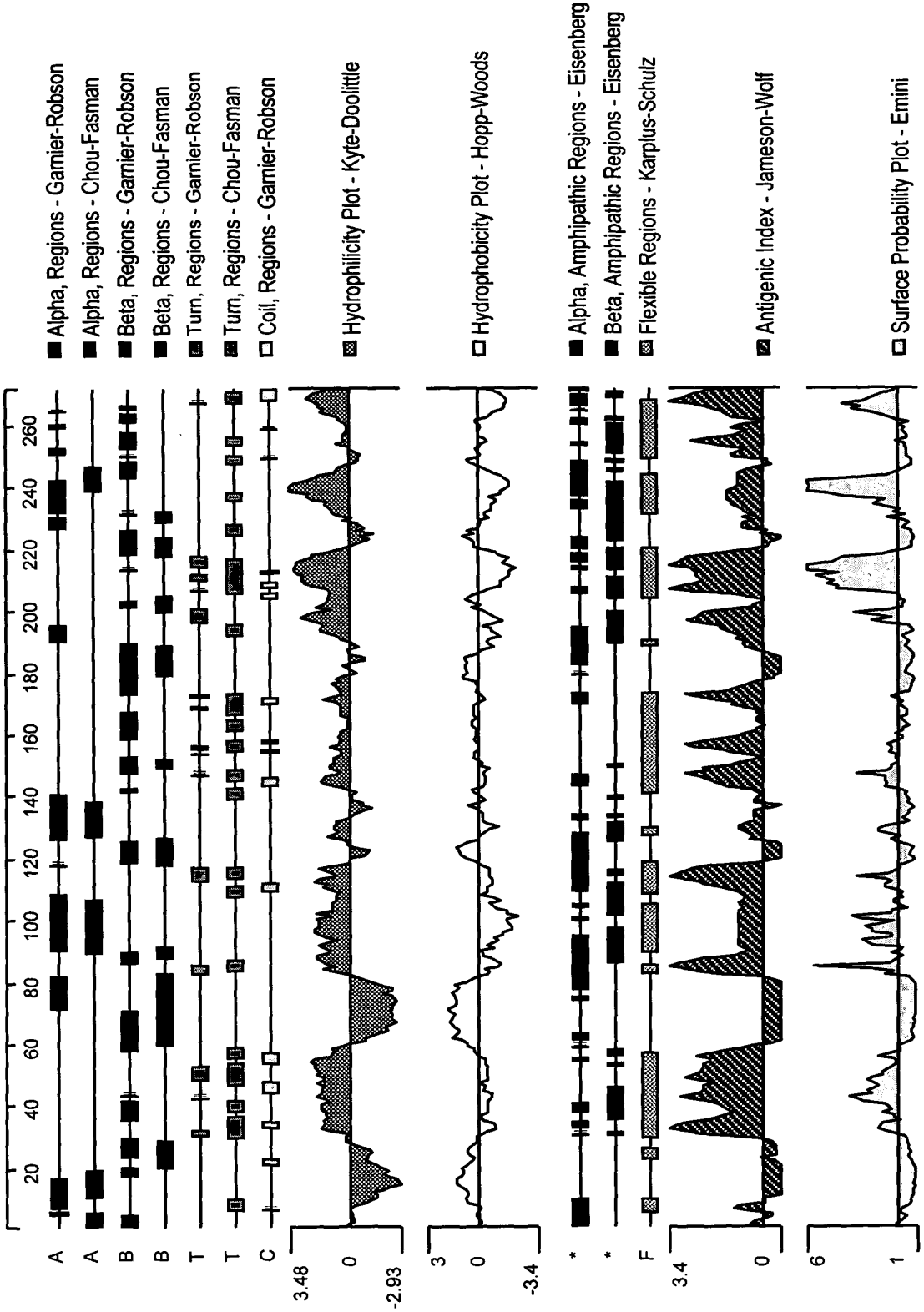

Alpha, Regions - Garnier-Robson
Alpha, Regions - Chou-Fasman
Beta, Regions - Garnier-Robson
Beta, Regions - Chou-Fasman
Turn, Regions - Garnier-Robson
Turn, Regions - Chou-Fasman
Coil, Regions - Garnier-Robson
Hydrophilicity Plot - Kyte-Doolittle
Hydrophobicity Plot - Hopp-Woods
Alpha, Amphipathic Regions - Eisenberg
Beta, Amphipathic Regions - Eisenberg
Flexible Regions - Karplus-Schulz
Antigenic Index - Jameson-Wolf
Surface Probability Plot - Emini
20 40 60 80 100 120 140 160 180 200 220 240 260
A A B B T T C
3.48 0 -2.93
3 0 -3.4
* * F
3.4 0
6 1

FIG. 5

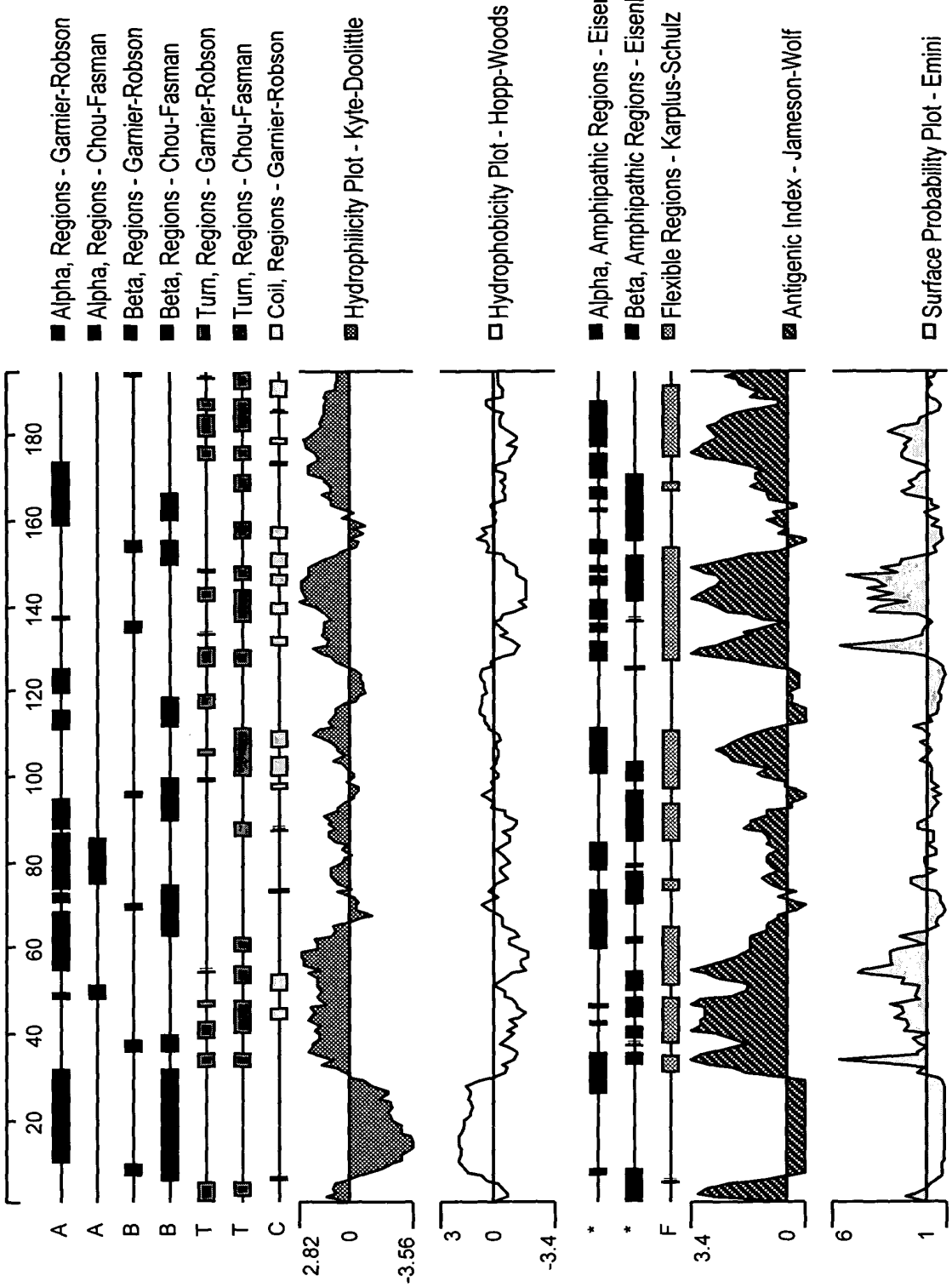

Alpha, Regions - Garnier-Robson
Alpha, Regions - Chou-Fasman
Beta, Regions - Garnier-Robson
Beta, Regions - Chou-Fasman
Turn, Regions - Garnier-Robson
Turn, Regions - Chou-Fasman
Coil, Regions - Garnier-Robson
Hydrophilicity Plot - Kyte-Doolittle
Hydrophobicity Plot - Hopp-Woods
Alpha, Amphipathic Regions - Eisenberg
Beta, Amphipathic Regions - Eisenberg
Flexible Regions - Karplus-Schulz
Antigenic Index - Jameson-Wolf
Surface Probability Plot - Emini
20
40
60
80
100
120
140
160
180
2.82
0
-3.56
3
0
-3.4
3.4
0
6
1

FIG. 6

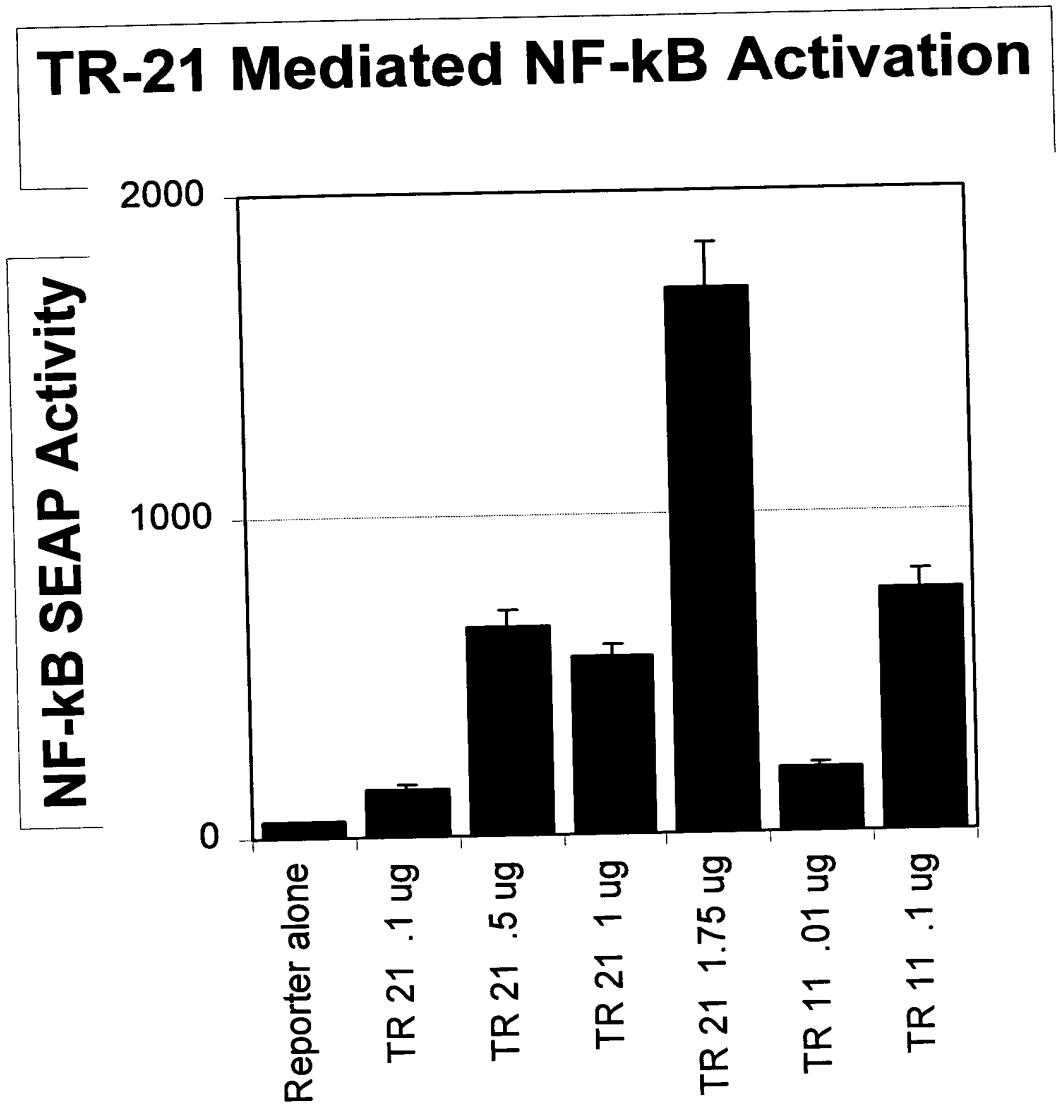

TR-21 Mediated NF-kB Activation
NF-kB SEAP Activity
2000
1000
0
Reporter alone
TR 21 .1 ug
TR 21 .5 ug
TR 21 1 ug
TR 21 1.75 ug
TR 11 .01 ug
TR 11 .1 ug

FIG. 7